

FIG. 1

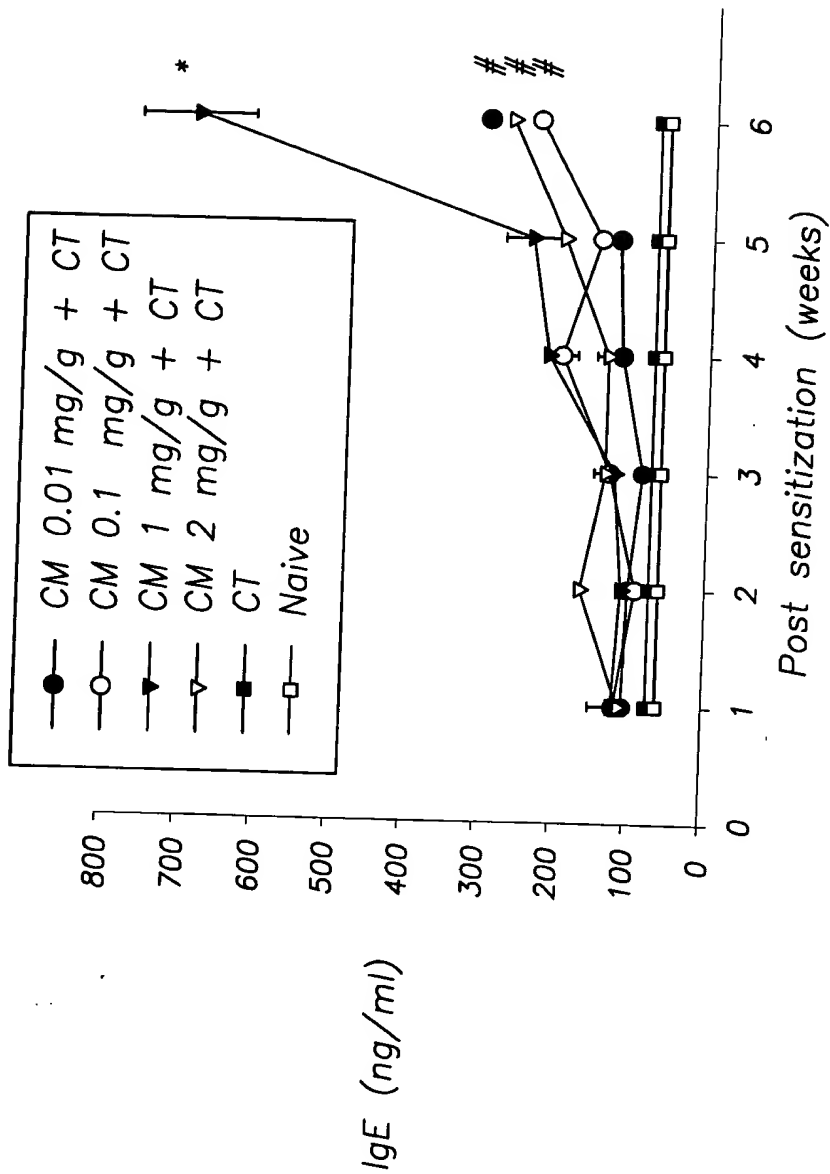
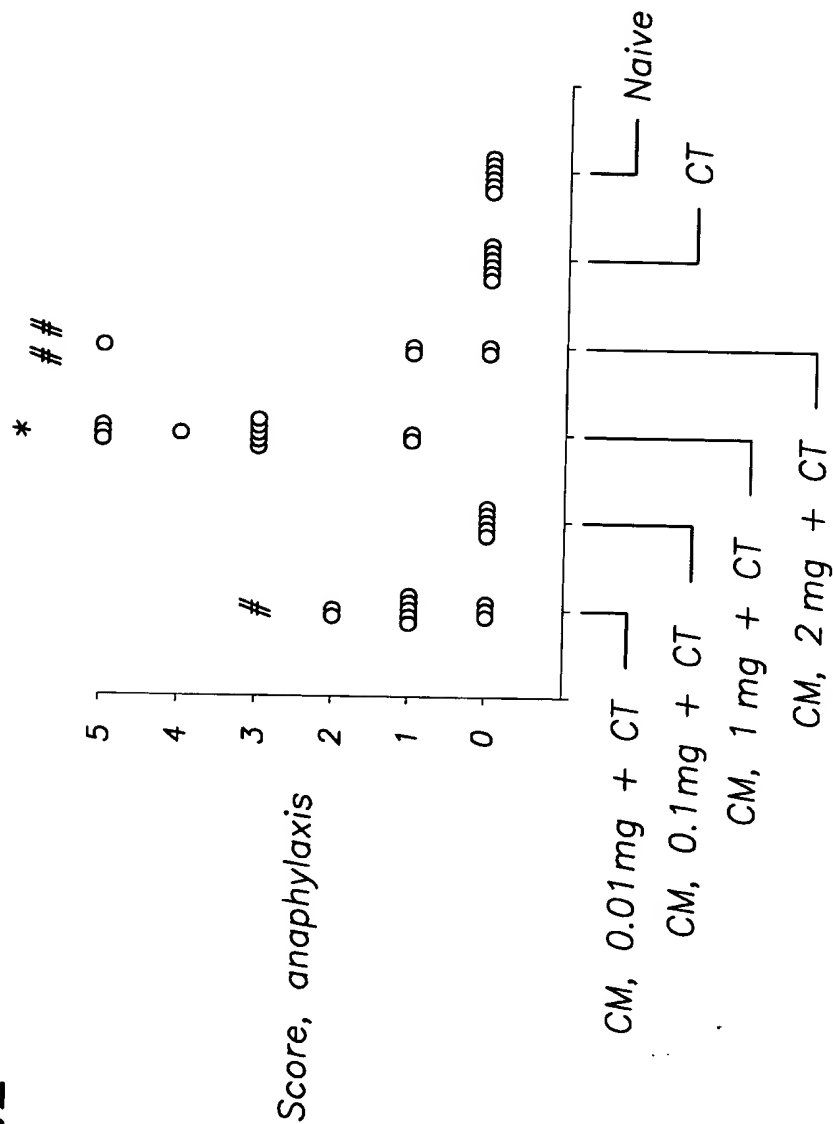


FIG. 2



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FIG. 3

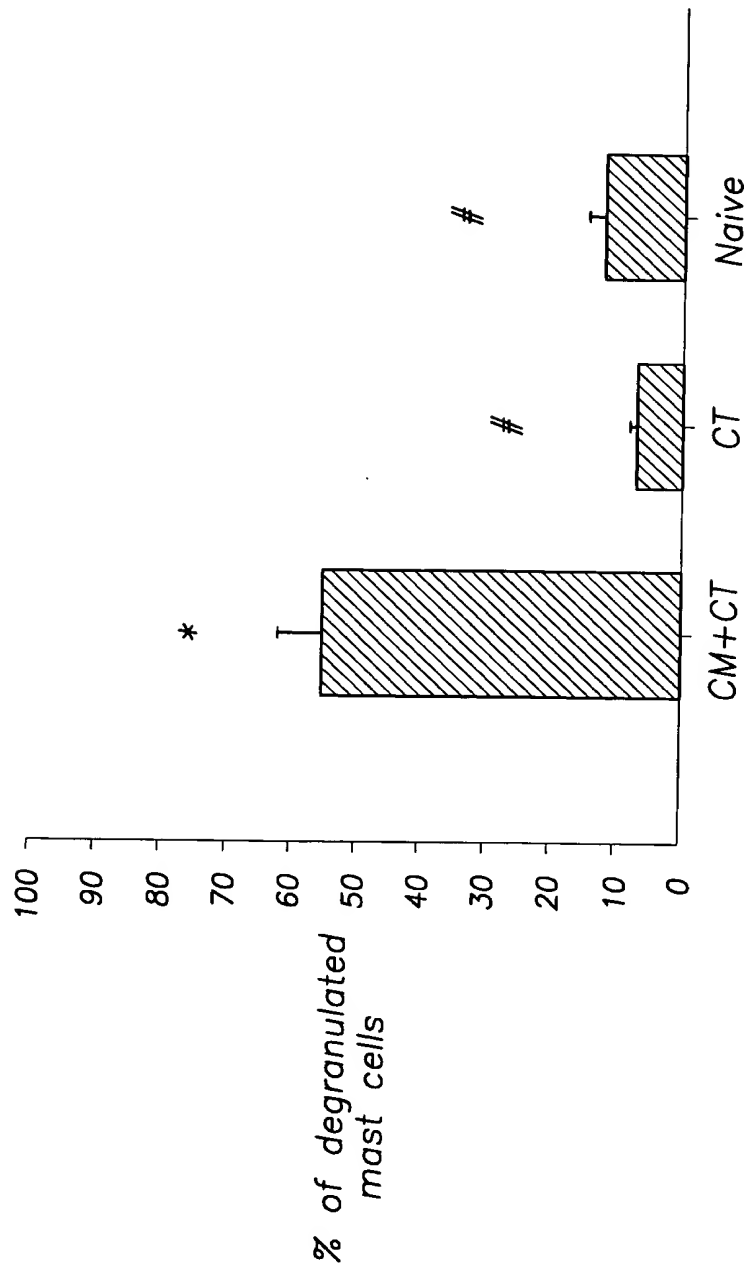


FIG. 4A (Week 3, first challenge)

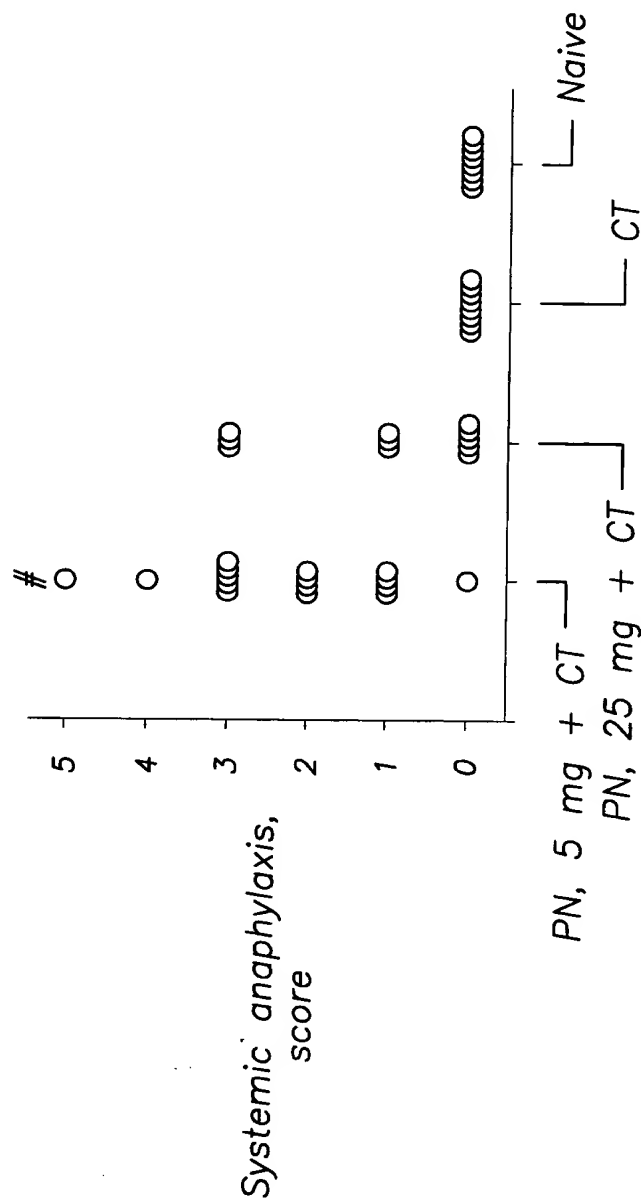
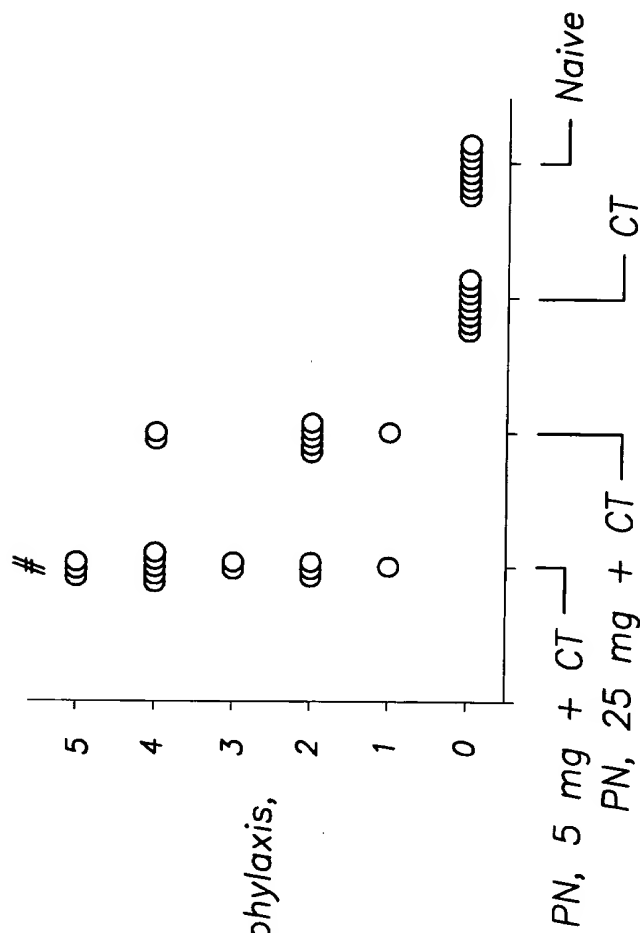


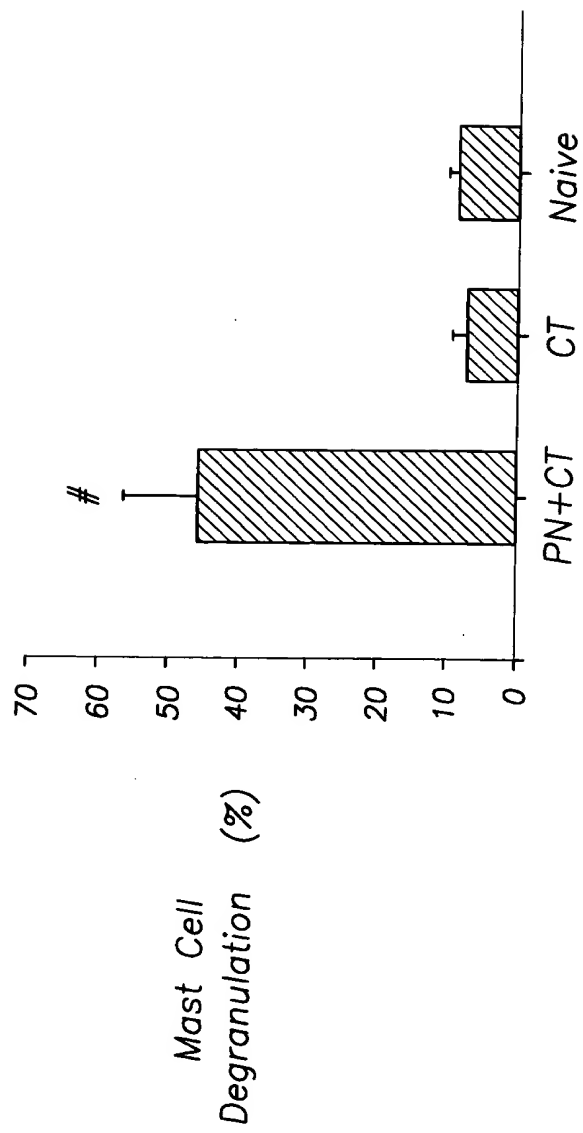
FIG. 4B (Week 5, re-challenge)

Systemic anaphylaxis,
score



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FIG. 5A



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FIG. 5B

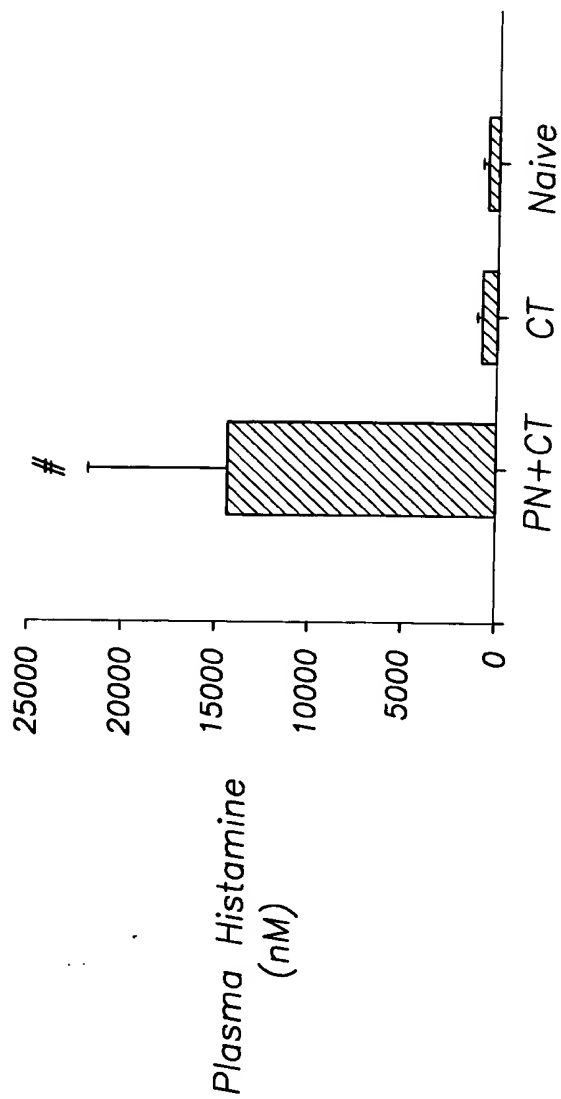
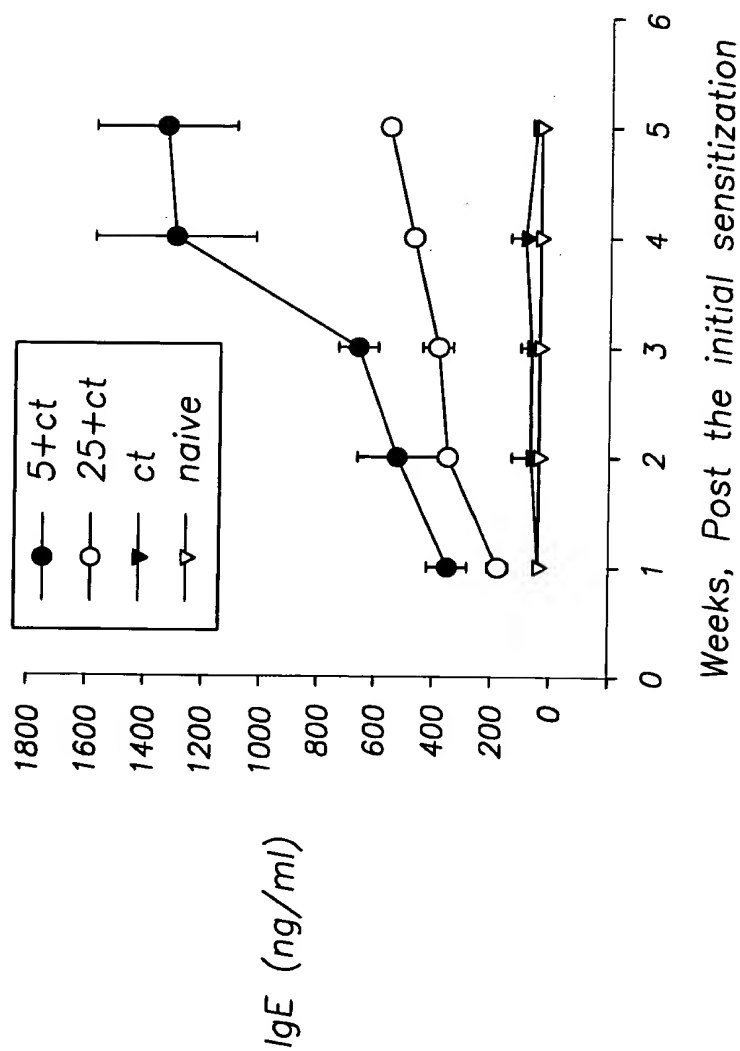
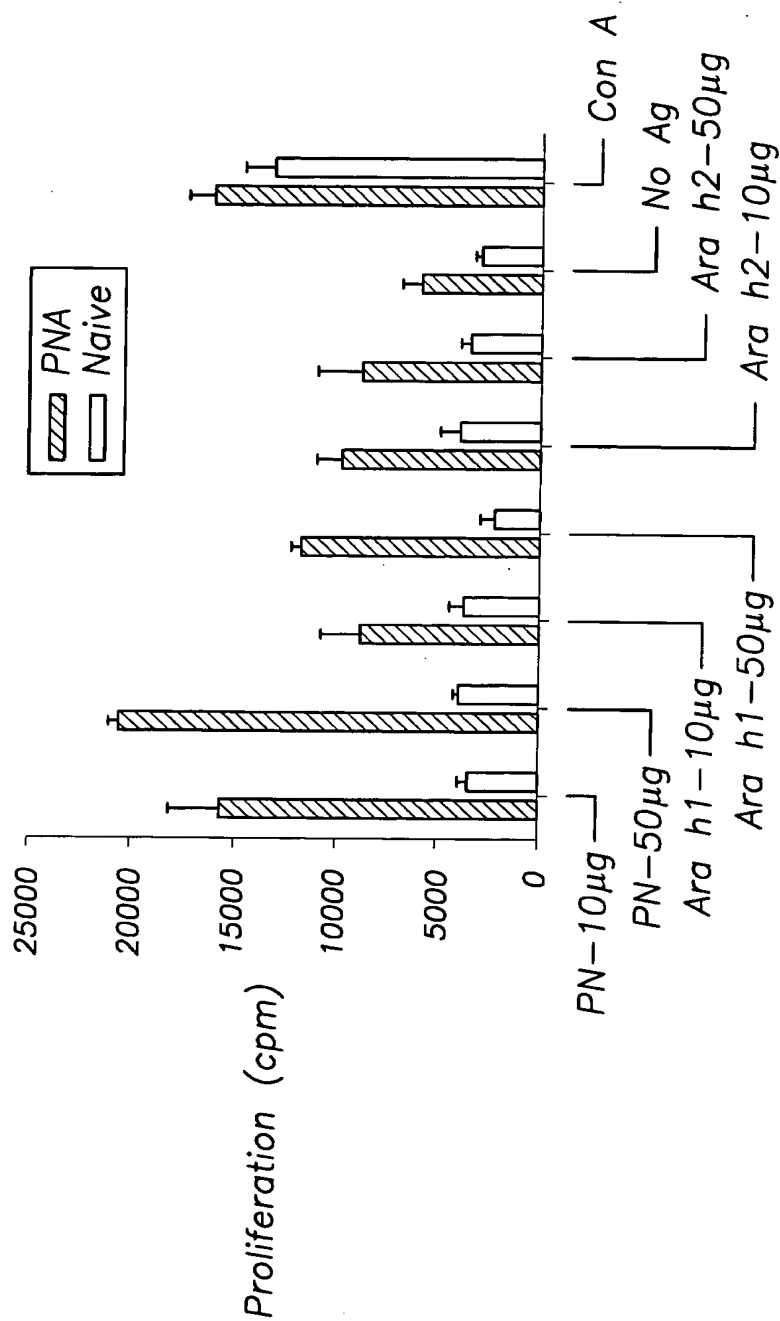


FIG. 6



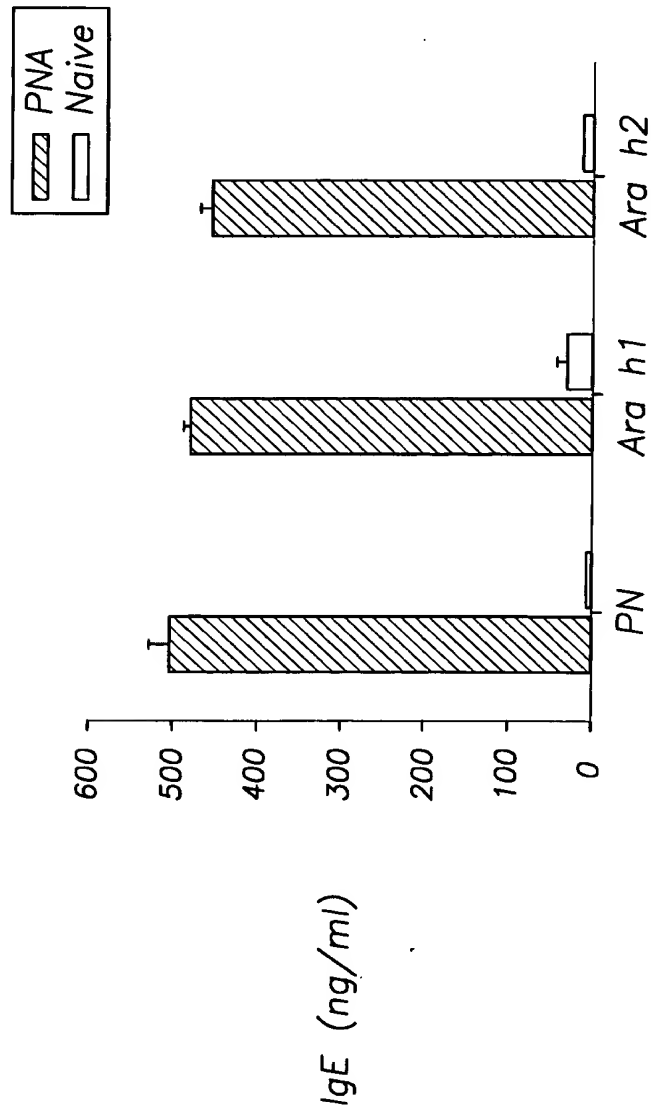
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FIG. 7



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FIG. 8



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FIG.9A

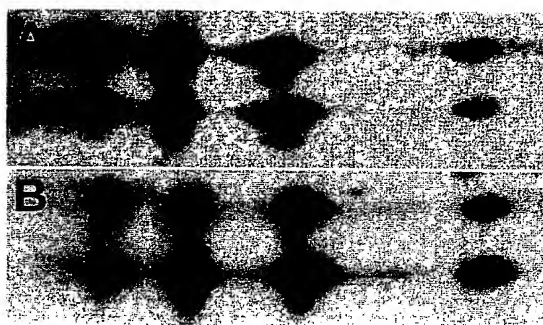


FIG.9B

FIG. 10A

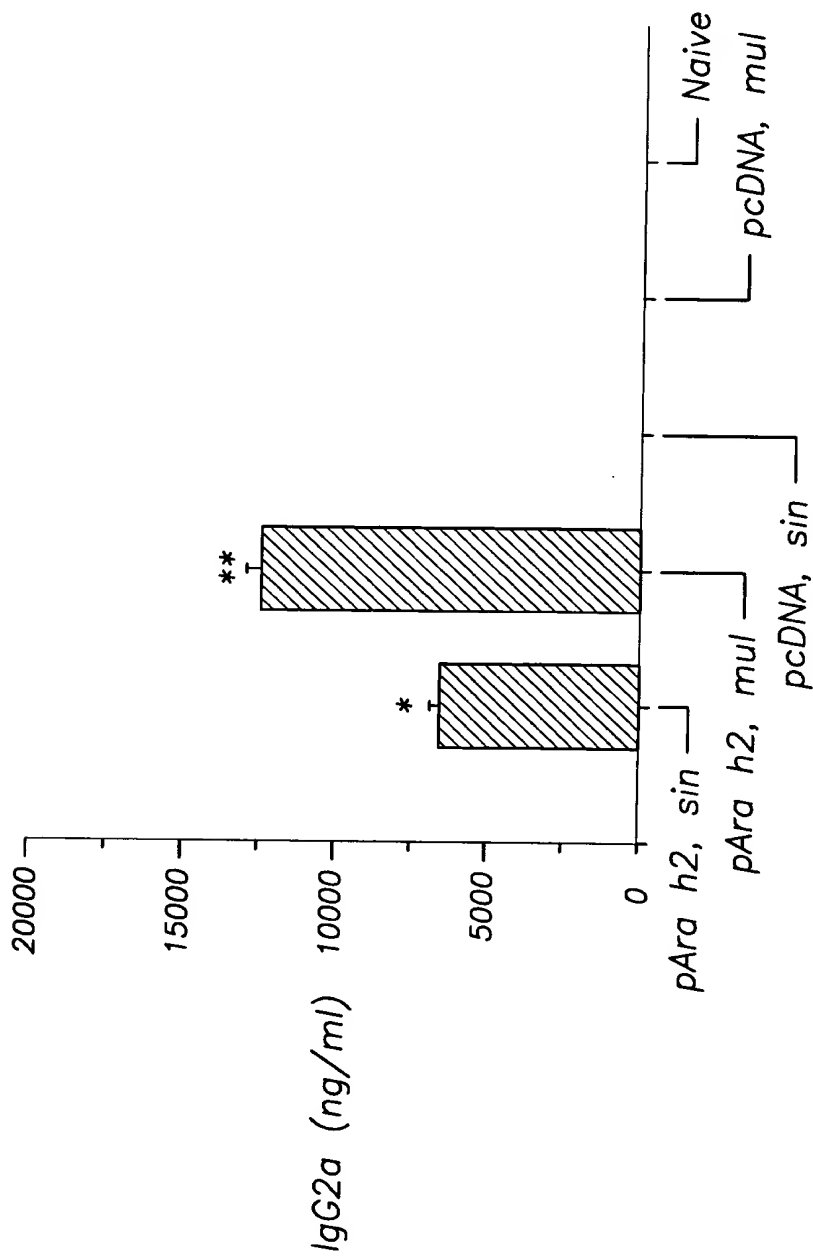


FIG. 10B

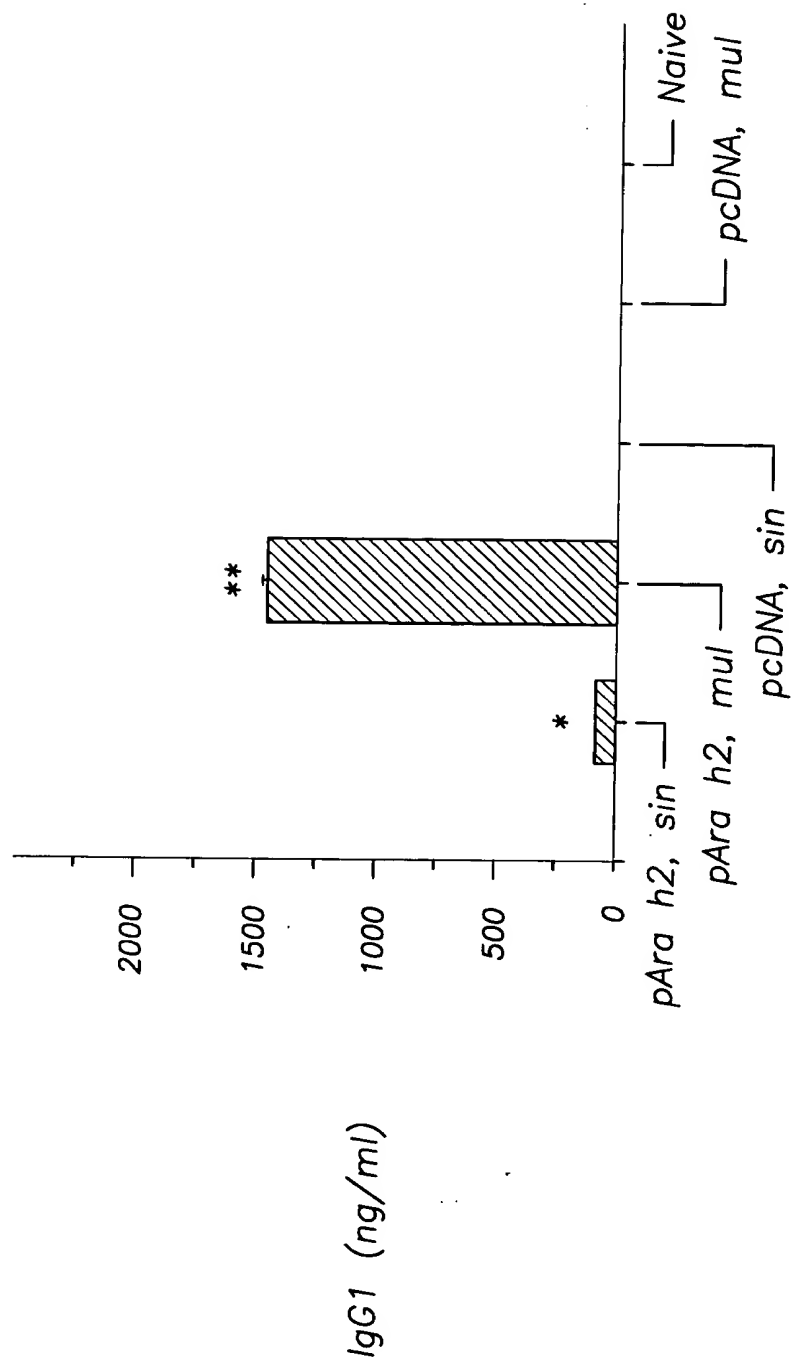


FIG. 11

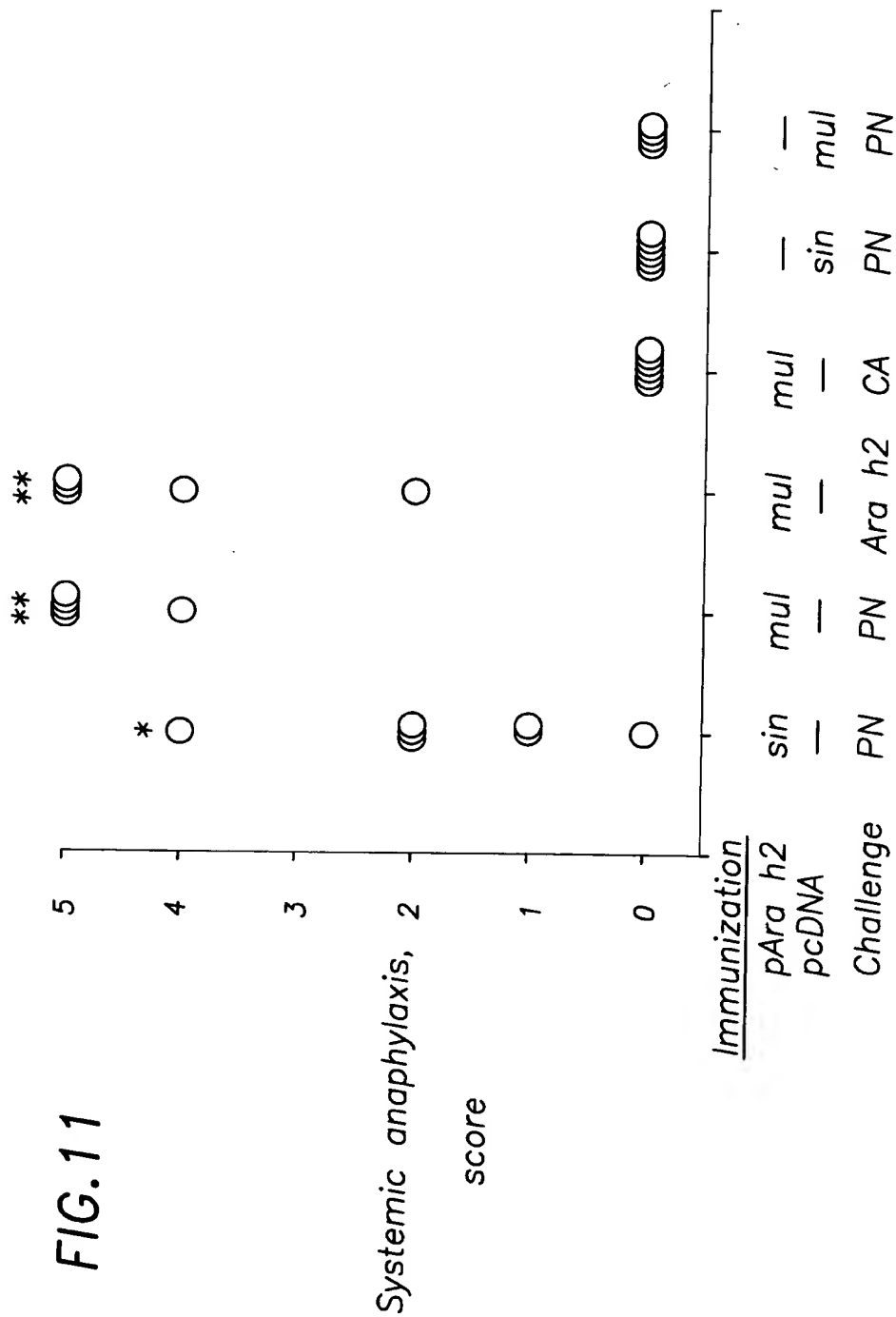


FIG.12

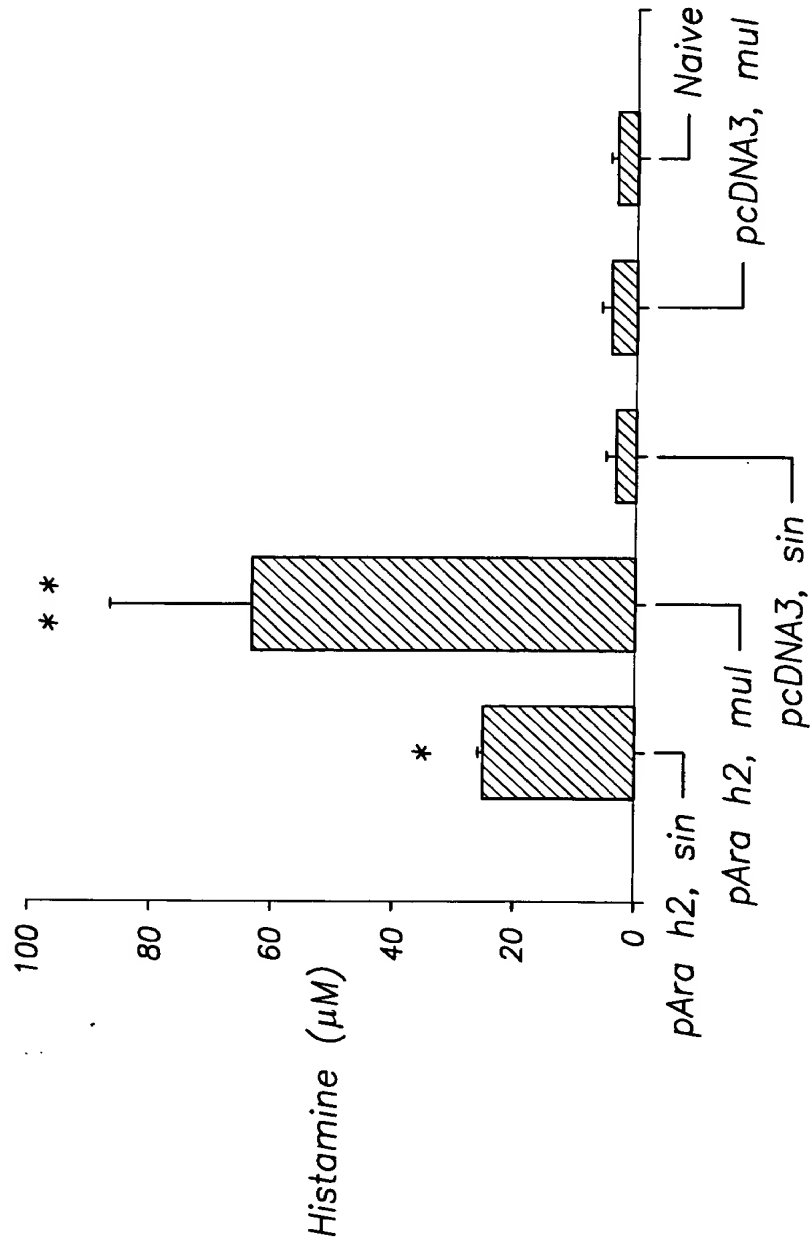


FIG. 13

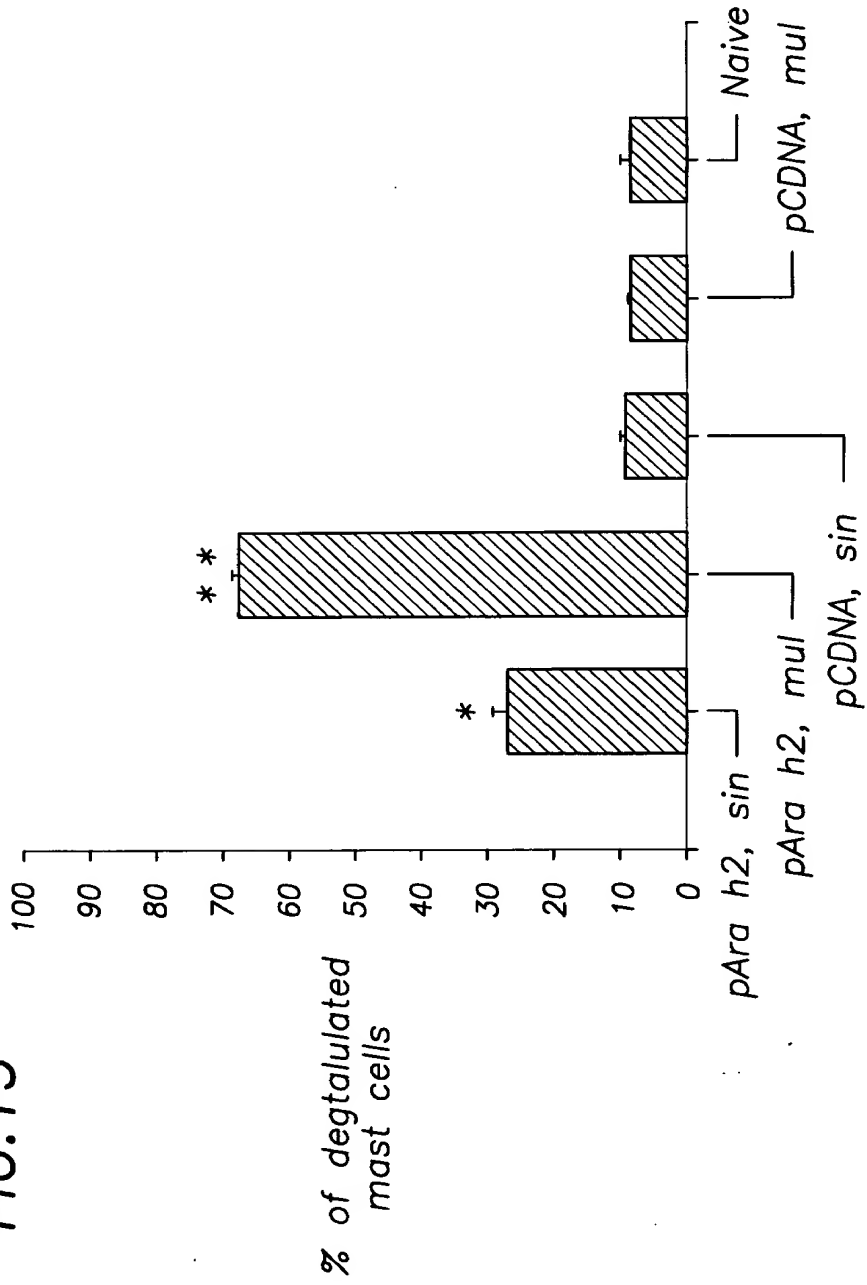


FIG. 14A

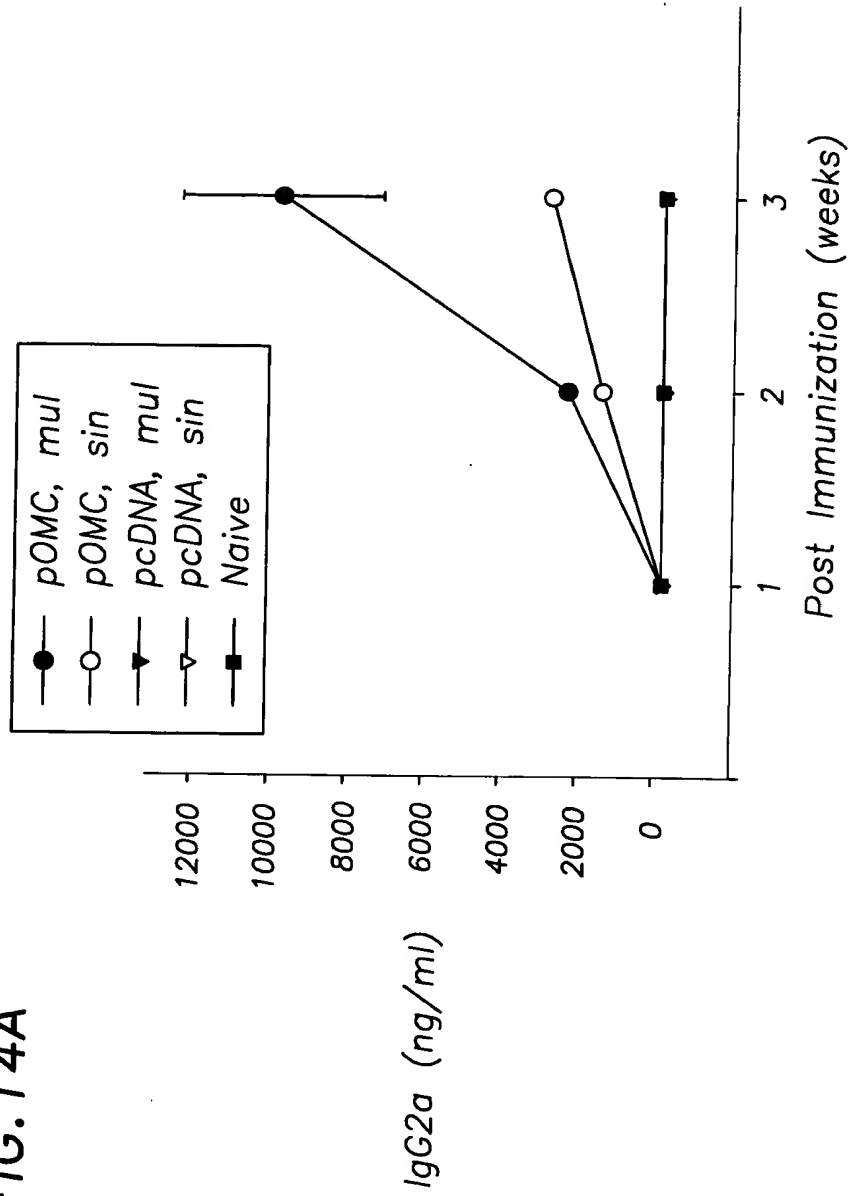
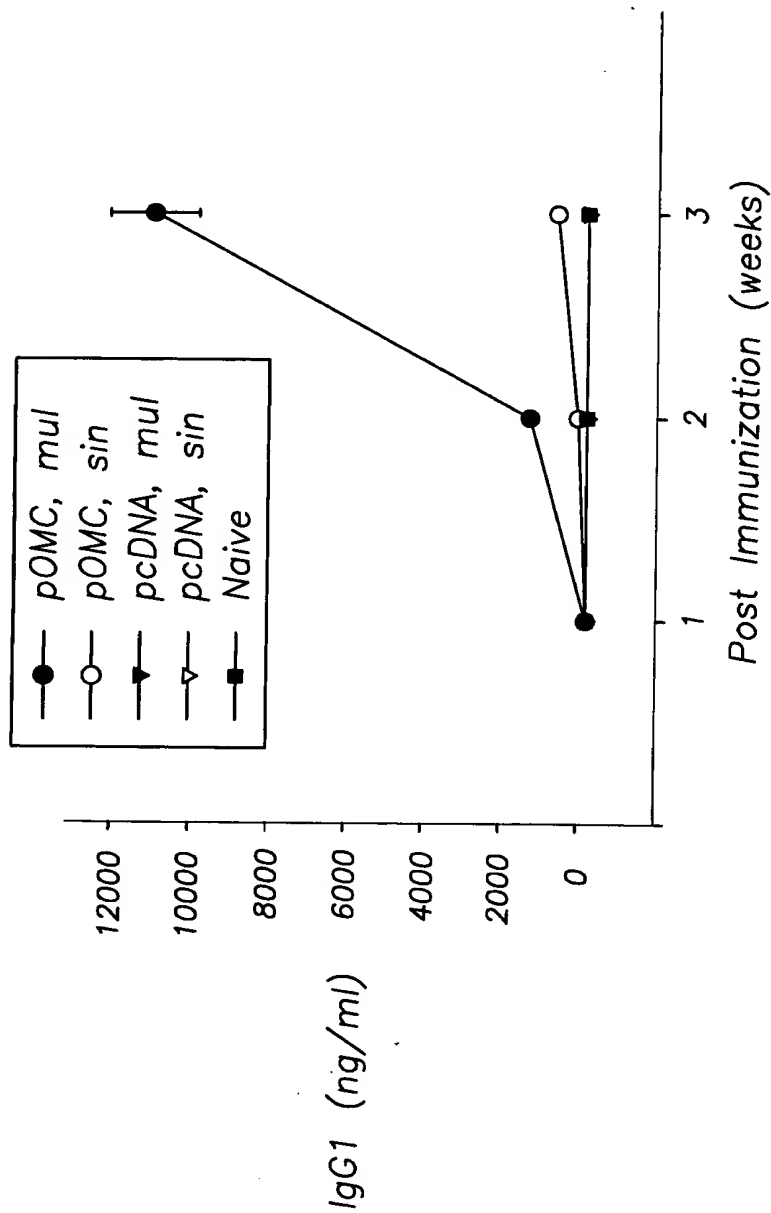


FIG. 14B

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lgG2a (ng/ml)

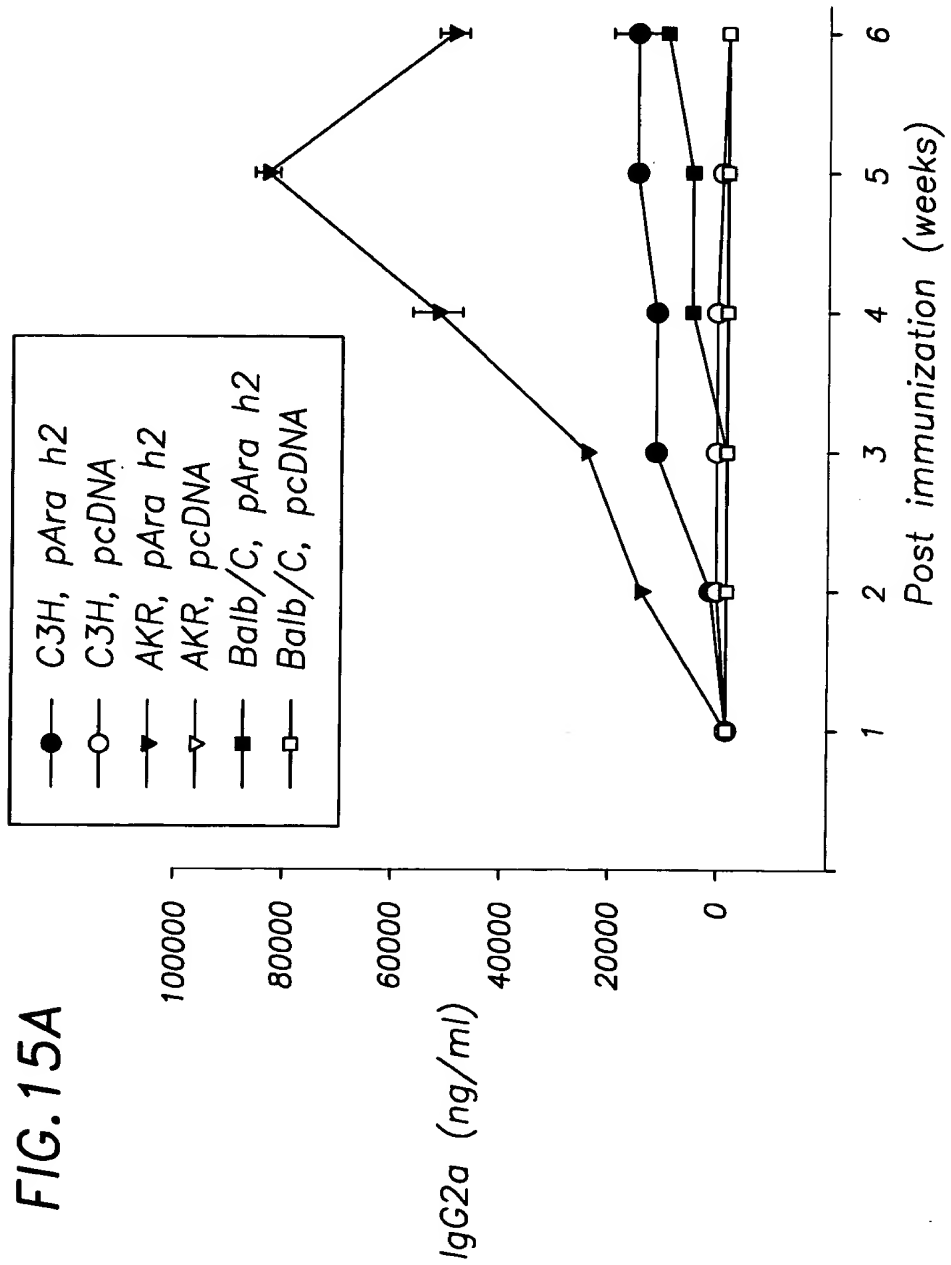


FIG. 15B

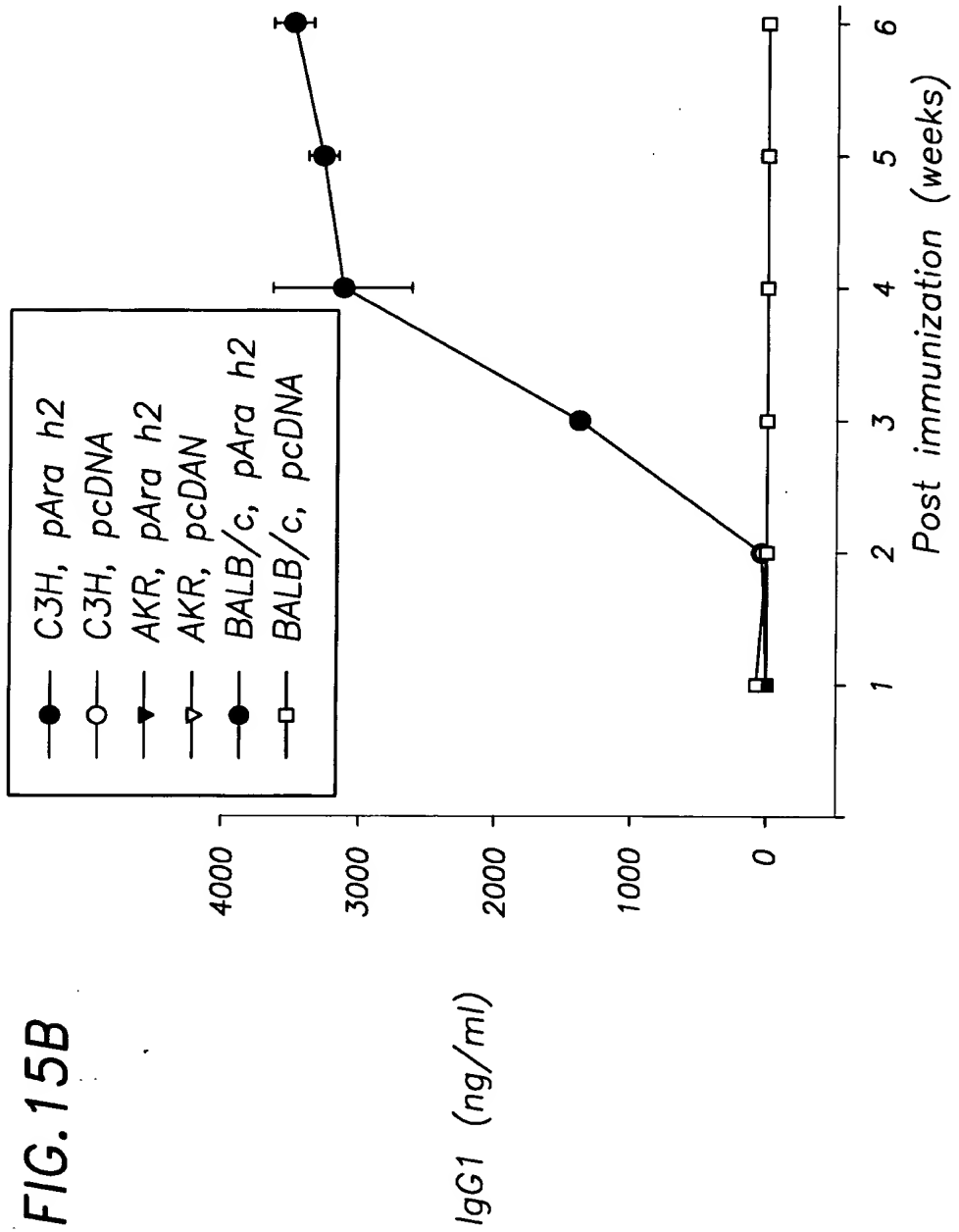


FIG.16A

PEPTIDE →	Ara h	#1	#2	#3	#4	#5	#6	#7	#8	#9	#10
PATIENT 1	5.3	0.9	2.9	3.8	7.8	0.9	0.9	0.7	1	0.9	0.7
PATIENT 2	4.3	0.7	1.4	1.3	2.4	0.9	0.8	0.7	0.7	1	0.7
PATIENT 3	2.8	1	1.8	1.6	2.4	1.1	1.1	1.4	1.7	1.3	1.3
PATIENT 4	1.8	1	0.6	0.8	2.1	1	0.5	0.7	1.4	0.7	0.8
PATIENT 5	5.5	2.1	1.1	0.7	0.8	1	1.3	0.7	1.5	0.5	0.6
PATIENT 6	20.8	1	1.6	2.2	1.7	1.4	1	1.8	2.7	2.6	1.2
PATIENT 7	1.5	0.7	0.5	0.7	0.9	0.9	0.7	0.9	1.1	0.8	0.7
PATIENT 8	6.5	2.4	1.2	1.3	1.1	0.9	1.1	1.4	0.8	0.9	0.8
PATIENT 9	9.2	1.1	1.1	6.3	1.2	1.5	1.2	1	1.2	1.3	0.8
PATIENT 10	11.7	0.7	0.6	0.7	0.6	1.3	0.5	0.6	0.9	0.6	0.5
PATIENT 11	2.1	0.7	0.7	0.5	0.6	0.5	0.3	0.6	0.5	0.5	0.5
PATIENT 12	1.1	1.4	1.6	1.8	2.8	1.5	1.5	1.4	1.3	1.5	1.2
PATIENT 13	0.9	1.3	1.9	1.9	2.8	2	1.6	2.4	1.9	1.5	1.5
PATIENT 14	4.8	1.2	1.6	1.5	1.9	1.6	1.9	1.3	1.6	1.8	1.3
PATIENT 15	6.9	0.7	1.1	1.8	2.1	1.1	1	1.1	1.1	1	0.8
PATIENT 16	10.2	0.7	1.6	2.7	10.9	2	0.9	2.1	2.1	1.4	1
PATIENT 17	4.2	1.4	1.6	2.8	2.6	1.3	1.4	1.7	1.6	1.1	1.3
PATIENT 18	3.9	1.5	1.7	2.9	3	1.5	1.2	1.3	1.3	1.9	1
PATIENT 19	3.4	1.5	1.2	2.6	1.4	1.7	0.9	1	1.4	1.2	1.1

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TO
FIG.16B

FIG. 16B

#11	#12	#13	#14	#15	#16	#17	#18	#19	#20	#21
0.9	1	0.8	1.2	0.9	1	1.2	1	5	7.3	6.6
0.7	0.6	0.5	1.1	0.7	0.7	0.7	0.5	1.9	4.3	3.4
1.7	0.9	0.9	1.3	1.2	1.4	1.2	1.1	1.1	1.4	1.4
0.7	0.5	0.6	1	1	0.7	0.7	0.7	1	1.4	1.6
0.7	0.3	0.8	0.8	0.7	0.5	0.5	0.6	4.4	2.2	1.6
1.4	1.2	1.2	1.1	0.9	0.7	1.4	3.9	0.6	0.7	0.9
1	1	0.7	0.8	1.1	1.1	0.7	1.2	1.2	1.4	1.4
1.2	1.3	1	1.2	1.4	1	1.1	3.5	1.3	1	1.2
0.8	1.5	0.9	0.8	0.9	1.1	0.7	1.9	1.4	1.3	1.4
0.5	0.8	0.7	0.4	0.5	0.7	0.7	0.6	1.6	1.2	1.1
0.8	0.5	0.7	0.7	0.4	0.4	0.7	0.6	0.6	0.5	0.8
1.1	1	1.1	1.4	1.4	1.1	1.3	1.2	1.3	1.9	2
1.7	1.9	1.4	1.2	1.5	1.3	1.5	2.3	1.6	1.3	1.8
1.1	1.3	0.9	0.9	1.2	1.1	1.5	5.1	3.5	2.2	2.1
1	1	1.2	1	0.7	1.2	1.4	2.2	1.2	1.1	1.4
0.8	0.9	0.8	0.6	0.8	0.7	0.7	1.6	3	2.5	5.8
1.2	1.7	1.7	1.1	1.7	1.5	1.6	1.2	1.4	1.2	1.3
1.3	1.2	0.9	1.7	1.7	1	1.6	2.1	3.4	3.8	6.3
1	1.3	1.1	1.4	1.6	1.3	1.3	1.3	1.4	1.5	1.7

FROM
FIG. 16A

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TO
FIG. 16C

FIG. 16C

#22	#23	#24	#25	#26	#27	#28	#29
6	3.4	4.6	6.4	7.5	5.1	11.3	0.9
3.6	1.4	1.4	1.5	1.9	1.5	2.2	0.5
2.1	1.1	0.7	1.2	1.2	1.3	0.9	1.2
2	1.2	1.1	1.4	1.4	1.5	1.1	0.6
2.5	1.4	1.7	1.9	2.2	1.7	3.3	0.5
0.8	1	0.7	0.9	0.6	0.7	1	1.5
2.3	1.5	1.6	1.3	1.5	1.4	1.8	0.6
1	1.1	1.8	1	1.1	1.5	1.3	1.3
0.5	1.5	1.5	1.2	1.2	1.6	1.1	2
1.3	1.3	0.7	1.5	1.3	1.5	1.4	0.6
0.6	0.6	0.7	0.7	0.8	0.8	0.5	0.5
1.5	1.3	1.3	1.7	1.8	1.1	1.3	1.4
1.6	1.5	1.7	1.6	1.7	2.2	1.3	1.4
1.9	1.6	1.5	2.8	3.3	2	2.7	1.1
1.4	0.9	1.2	1.5	1.5	1.4	1.1	0.9
16.8	1.4	1.7	4.9	3.3	5.3	12.1	1.4
1.7	1.2	1.2	1.9	1.6	1.4	2.9	1.2
7	1.6	1.8	2.7	3.5	4.3	5.1	1.6
2.4	1.4	1.6	1.5	1.3	1.2	1.7	0.9

FROM
FIG. 16B

FIG.17A

Modified Ara h 1:

MASMTGGOMGRDPNSS THAKSSPYQAKT ENPCAQRCLQSCQQEPDALK
QKACESRCKLEYDPRCAYDPRGHTGTTNQRSPPG[~]EATRGRQPGDYDDARRQPPRAEEGGR
WGPA[~]GP[~]REREREEDARQ[~]PREDWARD[~]PSHQQPRKARPEGREG[~]EQEWGTPGSHVREETSRNNP
FYF[~]PSRRFSTRYGNQNGRIRVLQRF[~]DQRSRQFQNLQNHRIVQIEAKPNTLVLPKHADADN
ILV[~]IQGQATVTVANGNNRKSFNLD[~]EGHALRIPSGFISYILNRHDNQNLRVAKISMPVNT
PGQ[~]MEDFFP[~]ASSRDQSSYLQGFARNTLEAAFN[~]AEANEIRRVLLEENAGGEQEARGQRRWS
TR[~]SSENNEGVIK[~]VSK[~]EHVEELTKHAKSVSKGSEEEGDITNPANLREGE[~]PDLSNNFGKL
AEVKPD[~]KKNPQLQDLDMMLTCVEIKEGALMLPHFNSKAMVIVVNKGTGNLELVAVRKEQ
QQRGRREEE[~]EDEDEEEGSGNREVRA[~]Y[~]TARLKEGDVFI[~]MPAAHPVAINASSELALLGFGIN
AENNHRIFLAGDADNVIDQIEKQAKALAA[~]PGSGEQVEKLKNQKESHFVAARPQSQSQSP
SSPEKESPEKEDQEEENQGGKG[~]PLLSILKAFN KLAAALEHHHHHH (SEQ ID NO. 109)

FIG.17B

Modified Ara h 2:

WASMTGGOMGRDPNS ARQQAELQGDRRCQ SQLARANLRACEAHL MQKI Q
AEDSYERAPYSPSQAPYSPSPYDRRGAGSSQHQERCCNELNEFENNQRC
MCEALQIMENQSDRLQGAQEQQFKREARNLPQQCGLRAPQRCDADVES
GGRDRY AAALEHHHHH (SEQ ID NO. 108)

FIG.17C

Modified Ara h 3:

M ASFRQQPEENACQFQRLNAQRPDNR IESEGGY IETWNANNQEFECAGV
ALSRLVLRNALRRPFYSNAPQE I F IQQGRGYFGL IFPGCPRHYEEPHTQGRRSQSQRPP
RRLQGEDQSQQQRD SHQKVHRFDEGDL I AVPTGVAFWL YNDHDTDVVAVSL TDINNNDNQ
LDQFPRRNLAGNTEQEF LRYQQQSRRRSLPYSYPSPQSPRQEEREFSPRGQHSRR
ERAGQEEENE^{EG}NI FSGFTPEAL FQAFQVDDRQ I VQNLRGETESEEEGA I VTVRGGLRAL
SPDRKRRADEEEYDEDEYAYDEEDRRRGRGSRGNGIEET I CTASAKNI GRNRS^{PD}I
YNPQAGSLKTANDLNL I LRWLGP^{SAE}YGNLYRNALFVAHYNTNAHS I YRLRGRAHVQV
VDSNGNRVYDEELQEGHVLVVPQNF^{AVAGK}SQSENFEYVAFKTD^{SRPS}I ANLAGENSVID
NLPEEVVANSYGLQREQARQLKNNNPFKFVPPSQSPRAVA VDKLAAL EHHHHH

(SEQ ID NO. 110)

FIG. 18

